

Amendments to the Claims

1-5. (cancelled)

6. (currently amended) A method of selecting a plant which compared to a wild type plant is impaired in transcriptional gene silencing, comprising
 - a) separately preparing RNA of a series of plants;
 - b) probing said RNA preparations with a nucleic acid which comprises ~~consists of~~ at least 50 nucleotide residues of a sequence that is at least 80% identical when aligned with a sequence selected from: ~~SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 27~~; and
 - c) identifying a plant whose RNA hybridizes with said nucleic acid.
7. (currently amended) The method of claim 6, wherein process steps b) and c) comprise reverse transcription of the RNA and subsequent amplification of the generated DNA using oligonucleotide primers specific for ~~SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9 or SEQ ID NO: 27~~.

8-12. (cancelled)

13. (currently amended) A kit for the identification of plants impaired in transcriptional gene silencing comprising: a nucleic acid which comprises ~~consists of~~ at least 50 nucleotide residues of a sequence that is at least 80% identical when aligned with a sequence selected from: ~~SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 27~~ conveniently which is then labeled to be used as a hybridization probe.

14-16. (cancelled)

17. (currently amended) A method according to claim 6 wherein said nucleic acid comprising ~~consists of~~ at least 100 nucleotide residues of a sequence that is at least 85% identical when aligned with a sequence selected from: ~~SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID~~

~~NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 27.~~

18. (currently amended) A method according to claim 6 wherein said nucleic acid comprises ~~consists of~~ at least 200 nucleotide residues of a sequence that is at least 90% identical when aligned with a sequence selected from: ~~SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 27.~~

19. (currently amended) A method ~~according to claim 6~~ wherein said nucleic acid ~~consists of~~ ~~SEQ ID NO: 7, SEQ ID NO: 9 or SEQ ID NO: 27~~ of selecting a plant which compared to a wild type plant is impaired in transcriptional gene silencing, comprising

- a) separately preparing RNA of a series of plants;
- b) probing said RNA preparations with a nucleic acid which consists of SEQ ID NO: 27;
and
- c) identifying a plant whose RNA hybridizes with said nucleic acid.

20. (new) The kit according to claim 13 wherein said nucleic acid comprises 100 nucleotide residues of a sequence that is at least 85% identical when aligned with SEQ ID NO:27 which nucleic acid is then labeled for use as a hybridization probe.

21. (New) The kit according to claim 20 wherein said nucleic acid comprises 200 nucleotide residues of a sequence that is at least 90% identical when aligned with SEQ ID NO:27 which nucleic acid is then labeled for use as a hybridization probe.